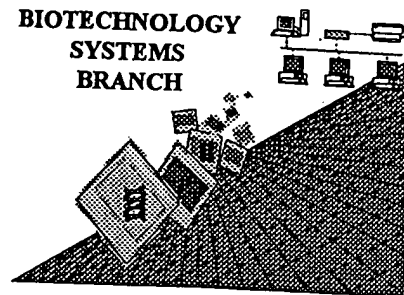


Wessendorf

RAW SEQUENCE LISTING ERROR REPORT



BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/013,077

Art Unit / Team No. : 1618

Date Processed by STIC: 8/25/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212



Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/013,077

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 J Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
 AKS-Biotechnology Systems Branch- 5/15/99

DATE: 08/25/1999
TIME: 09:29:57

PAGE: 1



RAW SEQUENCE LISTING
PATENT APPLICATION US/09/013,077

INPUT SET: S33047.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

IMPORTANT:
See item 5
on Enn Summary
Sheet

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: REID, ROBERT H.
- 6 SADEGH-NASSERI, SCHEHERAZADE
- 7 WOLFF, MARCIA
- 8 NAUSS, JEFFREY L.
- 9
- 10 (ii) TITLE OF INVENTION: MODEL FOR TESTING IMMUNOGENICITY OF PEPTIDES
- 11
- 12 (iii) NUMBER OF SEQUENCES: 15
- 13
- 14 (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: WERTEN BELLAMY, ESQ., OFFICE OF JUDGE
- 16 ADVOCATE GENERAL, ARMY
- 17 (B) STREET: 901 NORTH STUART STREET
- 18 (C) CITY: ARLINGTON
- 19 (D) STATE: VA
- 20 (E) COUNTRY: USA
- 21 (F) ZIP: 22203
- 22
- 23 (v) COMPUTER READABLE FORM:
- 24 (A) MEDIUM TYPE: Floppy disk
- 25 (B) COMPUTER: IBM PC compatible
- 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 27 (D) SOFTWARE: Patentln Release #1.0, Version #1.25
- 28
- 29 (vi) CURRENT APPLICATION DATA:
- 30 (A) APPLICATION NUMBER: US 08/247,884
- 31 (B) FILING DATE: 23-MAY-1994
- 32 (C) CLASSIFICATION:
- 33
- 34 (viii) ATTORNEY/AGENT INFORMATION:
- 35 (A) NAME: BELLAMY, WERTEN F.W.
- 36 (B) REGISTRATION NUMEER: 27,029
- 37 (C) REFERENCE/DOCKET NUMBER: 252.32966PX1
- 38
- 39 (ix) TELECOMMUNICATION INFORMATION:
- 40 (A) TELEPHONE: 703-696-8119
- 41 (B) TELEFAX: 703-696-8116
- 42
- 43

ERRORED SEQUENCES FOLLOW:

US ← all upper-case letters
There go under PRIOR APPLICATION DATA: section

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/013,077

DATE: 08/25/1999

TIME: 09:29:57

INPUT SET: S33047.raw

44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:
47 (A) LENGTH: 13 amino acids
48 (B) TYPE: amino acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: peptide
53 (iii) HYPOTHETICAL: NO
54
55 (iv) ANTI-SENSE: NO
56
57 (v) FRAGMENT TYPE: internal
58
59
60
--> 61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1
62
63 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
64 1 5 10
65

1 ← use numeral 1, not lower-case "l"

108 (2) INFORMATION FOR SEQ ID NO:4:
109
110 (i) SEQUENCE CHARACTERISTICS:
--> 111 (A) LENGTH: 13 amino acids
112 (B) TYPE: amino acid
113 (C) STRANDEDNESS: single
114 (D) TOPOLOGY: linear
115
116 (ii) MOLECULE TYPE: peptide
117 (iii) HYPOTHETICAL: NO
118
119 (iv) ANTI-SENSE: NO
120
121 (v) FRAGMENT TYPE: internal
122
123
124
125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
--> 126 Val Gly Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro
127 1 5 10

invalid

--> 232 (2) INFORMATION FOR SEQ ID NO:10:
233
234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 13 amino acids
236 (B) TYPE: amino acid
237 (C) STRANDEDNESS: single
238 (D) TOPOLOGY: linear
239
240 (ii) MOLECULE TYPE: peptide

use numeral "1"

RAW SEQUENCE LISTING PATENT APPLICATION US/09/013,077

DATE: 08/25/1999

TIME: 09:29:58

INPUT SET: S33047.raw

241 (iii) HYPOTHETICAL: NO
242 (iv) ANTI-SENSE: NO
243
244 (v) FRAGMENT TYPE: internal
245
246
--> 247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
248
249 Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu
250 1 5 10
251

use numeral "0", not upper-case "O"

347 (2) INFORMATION FOR SEQ ID NO:14:
348
349 (i) SEQUENCE CHARACTERISTICS:
--> 350 (A) LENGTH: 82 amino acids
351 (B) TYPE: amino acid
352 (C) STRANDEDNESS: single
353 (D) TOPOLOGY: linear
354
355 (ii) MOLECULE TYPE: peptide
356 (iii) HYPOTHETICAL: NO
357 (iv) ANTI-SENSE: NO
358
359 (v) FRAGMENT TYPE: N-terminal
360
361
362 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
363
364 Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro
365 1 5 10 15
366
367 Asp Gln Ser Gly Glu Met Phe Asp Phe Asp Gly Asp Glu Ile Phe
368 20 25 30
369
370 His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe
371 35 40 45
372
373 Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala
374 50 55 60
375
376 Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr
377 65 70 75 80
378 Pro Ile
379 80
380

81 shown

numbering off

381 (2) INFORMATION FOR SEQ ID NO:15:
382
383 (i) SEQUENCE CHARACTERISTICS:
384 (A) LENGTH: 96 amino acids
385 (B) TYPE: amino acid
386 (C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/013,077DATE: 08/25/1999
TIME: 09:29:58

INPUT SET: S33047.raw

387 (D) TOPOLOGY: linear
388
389 (ii) MOLECULE TYPE: peptide
390 (iii) HYPOTHETICAL: No
391 (iv) ANTI-SENSE: NO
392
393 (v) FRAGMENT TYPE: C-terminal
394
395
396
397 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
398
399 Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His
400 1 5 10 15
401
402 Phe Phe Asn Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr
403 20 25 30
404
405 Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg
406 35 40 45
407
408 Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln
409 50 55 60
410
411 Lys Asp Leu Leu Glu Gln Arg Arg Arg Ala Val Asp Thr Tyr Cys Arg
412 65 70 75 80
413
414 His Met Tyr Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val His
415 85 90 95
416
417
418
419
420
421
422
423
424
425

-->

??

delete at end of file

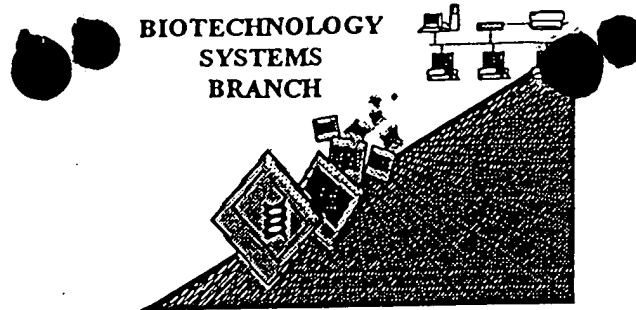
SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/013,077

DATE: 08/25/1999

TIME: 09:29:59

INPUT SET: S33047.raw

Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: Us 08/247,884
61	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
111	Entered (13) and Calc. Seq. Length (12) differ	(A) LENGTH: 13 amino acids
126	Wrong Amino Acid Designator	Val Gly Lye Asn Ile Thr Val Thr Ala Ser Val Asp Pro
232	Invalid Character at Sequence Number Position	(2) INFORMATION FOR SEQ ID NO:10:
247	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
350	Entered (82) and Calc. Seq. Length (81) differ	(A) LENGTH: 82 amino acids
416	Wrong Amino Acid Designator	??



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: `pub/checker/`
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

COST FOR DISKETTE IS \$ 25.00

METHOD OF PAYMENT:

Check payable to Commissioner of Patents and Trademarks
VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737
PTO Deposit Account

For Further Information, Contact: Arti Shah at 703-308-4212